ABSTRACT OF THE DISCLOSURE

Disclosed is a method of specifically amplifying desired regions of nucleic acid from a sample containing nucleic acid. The method includes providing a plurality of first PCR primers, each first primer having a region of fixed nucleotide sequence identical or complementary to a consensus sequence of interest and a region of randomized nucleotide sequence located 5' to, 3' to, anywhere within, or flanking the region of fixed nucleotide sequence; providing a plurality of second PCR primers, each second primer having a region of arbitrary, yet fixed nucleotide sequence and a region of randomized nucleotide sequence located 5' to, 3' to, anywhere within, or flanking the region of fixed nucleotide sequence; and then amplifying the nucleic acid present in the sample via the PCR using the plurality of first PCR primers and the plurality of second PCR primers; whereby a subset of the plurality first primers binds to the consensus sequence of interest substantially wherever it occurs in the sample, and a subset of the plurality of second primers binds to the sample at locations removed from the first primers such that DNA regions flanked by the first primer and the second primer are specifically amplified.